CLAIMS:

1. A method of searching for a plurality of query sequences in a set of target sequence fragments, allowing for mismatches at up to **n** sequence positions, comprising the steps of:

a) logically dividing each query sequence and each target fragment into at least **n+1** segments;

b) for each query sequence, constructing a first and a second query group by distributing the query sequence segments there between such that at least **n** segments are contained in the second query group;

c) constructing from each target fragment a first target group having the same segment distribution as the first query group; and

d) for each query sequence, comparing said first query group with each first target group to identify potential matching target fragments.

2. The method of claim 1 wherein steps (b) to (d) are repeated using different distributions of segments between said query groups.

3. The method of claim 2 wherein steps (b) to (d) are repeated using all distinct distributions of segments between said query groups.

4. The method of any preceding claim further comprising, for each potential matching target fragment identified in step (d), the following steps:

(e) constructing a second target group having the same segment distribution as the second query group of the potentially matching query sequence; and

(f) comparing said second query group with said second target group to identify a match, allowing for mismatches in up to **n** sequence positions.

5. The method of claim 4 wherein step (f) is carried out by applying an exclusive OR operation to binary representations of the second query group and second target group.

6. The method of claim 5 wherein the result of said exclusive OR operation is analysed using a lookup table.

7. The method of any preceding claim further comprising, for each distinct distribution of query sequence segments, constructing a first query table indexed by possible values of the first query groups, the entries in the first query table providing access to each second query group by using as an index the value of a corresponding first query group.

8. The method of claim 7 further comprising, for each distinct distribution of query sequence segments, constructing a second query table providing access to each second query group, the entries in the first query table providing references to appropriate entries in the second query table.

9. The method of claim 7 or 8 further comprising the step of, for each first target group constructed in step (c),

implementing step (d) by using said first target group to form an index into said first query table.

10. The method of claim 7, 8 or 9 wherein, if two distinct distributions of query sequence segments are such that the first query group of one distribution is the same as the second query group of the other distribution, said query tables for both of the distinct distributions are constructed and/or used concurrently.

11. The method of any preceding claim wherein said target sequence fragments comprise overlapping fragments of one or more target sequences.

12. The method of any preceding claim wherein said query sequences and target sequence fragments comprise biochemical sequence data.

13. The method of claim 12 wherein said query sequences and target sequence fragments are binary encoded.

14. The method of any preceding claim wherein **n** is at least two.

15. The method of any preceding claim wherein said query sequences and target sequence fragments are logically divided into an even number of segments, and the segments are distributed in equal numbers between the first and second query and target groups.

16. Computer apparatus comprising elements adapted to carry out the method of any preceding claim.

17. A computer program product carrying computer program code comprising elements adapted to carry out the method of any of claims 1 to 15 when executed on a computer.

18. A computer readable medium comprising computer program code adapted to carry out the method steps of any of claims 1 to 15 when executed on a computer.

19. Computer apparatus comprising a memory, for searching for a plurality of query sequences in a set of target sequence fragments, allowing for mismatches at up to **n** sequence positions comprising:

a query groups constructor adapted to construct in the memory, for each query sequence, first and second query groups by logically dividing each query sequence into **n+1** segments and distributing the query sequence segments between the first and second query groups in one or more ways such that at least **n** segments are contained in each second query group;

a target groups constructor adapted to construct in the memory, for each target sequence fragment, one or more first target groups having segment distributions corresponding to the first query groups; and

a first group comparator adapted, for each query sequence, to compare said one or more first query groups with corresponding ones of said one or more first target groups and to thereby output a result identifying potentially matching query sequences and target fragments.

20. The apparatus of claim 19, wherein the query groups constructor and target groups constructor are adapted to

construct, for each query sequence and target fragment respectively, a plurality of groups having all distinct distributions of segments between said first and second groups.

21. The apparatus of claim 19 or 20 wherein the target groups constructor is adapted to construct, at least for each target sequence fragment identified by the first group comparator as a potentially matching target fragment, one or more second target groups having segment distributions corresponding to the second query groups, and further comprising a second group comparator adapted, for each identified potentially matching query group and target fragment, to compare the corresponding second query group and second target group to identify a match allowing for mismatches in up to **n** sequence positions.

22. The apparatus of any of claims 19 to 21, further adapted, for each distinct distribution of query sequence segments, to construct in the memory a first query table indexed by possible values of the first query groups, the entries in the first query table providing access to each second query group by using as an index the value of a corresponding first query group.

23. The apparatus of claim 22 further adapted, for each distinct distribution of query sequence segments, to construct in the memory a second query table providing access to each second query group, the entries in the first query table providing references to appropriate entries in the second query table.

24. A computer program product comprising computer program code for searching for a plurality of query sequences in a set of target sequence fragments, allowing for mismatches at up to **n** sequence positions comprising:

a query groups constructor adapted to construct in the memory, for each query sequence, first and second query groups by logically dividing each query sequence into **n+1** segments and distributing the query sequence segments between the first and second query groups in one or more ways such that at least **n** segments are contained in each second query group;

a target groups constructor adapted to construct in the memory, for each target sequence fragment, one or more first target groups having segment distributions corresponding to the first query groups; and

a first group comparator adapted, for each query sequence, to compare said one or more first query groups with corresponding ones of said one or more first target groups and to thereby output a result identifying potentially matching query sequences and target fragments.